Amendments to the Claims

This listing of claims replaces all prior versions, and listings, of the claims in the application.

Listing of Claims:

Claims 1-115 (Canceled)

116. (Currently Amended) A detection probe for use in determining the presence of SARS-CoV in a test sample, said probe ~~being up to 100 bases in length and~~ comprising a target binding portion ~~which forms a hybrid stable for detection with a target sequence contained within~~ that is perfectly complementary to all or a portion of a target sequence consisting of the base sequence of SEQ ID NO:3 or its complement,

wherein said target binding region forms a hybrid stable for detection with said target sequence under stringent hybridization conditions,

wherein said probe does not comprise any other base sequences which stably hybridize to nucleic acid derived from SARS-CoV under said conditions, and

wherein said probe does not form a hybrid stable for detection with nucleic acid derived from HCoV-OC43 or HCoV-229E under said conditions.

117. (Previously Presented) The probe of claim 116, wherein said target binding portion comprises an at least 10 contiguous base region which is perfectly complementary to an at least 10 contiguous base region of SEQ ID NO:3 or its complement.

118. (Previously Presented) The probe of claim 116, wherein said target binding portion comprises an at least 15 contiguous base region which is perfectly complementary to an at least 15 contiguous base region of SEQ ID NO:3 or its complement.

119. (Previously Presented) The probe of claim 116, wherein said target binding portion comprises an at least 18 contiguous base region which is perfectly complementary to an at least 18 contiguous base region of SEQ ID NO:3 or its complement.

Claims 120-123 (Canceled)

124. (Previously Presented) The probe of claim 116, wherein the base sequence of said probe is perfectly complementary to all or a portion of the base sequence of SEQ ID NO:3 or its complement.

125. (Previously Presented) The probe of claim 116, wherein the base sequence of said probe is perfectly complementary to 18 to 23 contiguous bases of the base sequence of SEQ ID NO:3 or its complement.

126. (Currently Amended) The probe of claim ~~120~~ 116, wherein said probe is a self-hybridizing probe under said conditions and in the absence of said target sequence.

127. (Previously Presented) The probe of claim 126, wherein said probe comprises a pair of interacting labels.

128. (Previously Presented) The probe of claim 127, wherein said pair of interacting labels is selected from the group consisting of a luminescent/quencher pair, a luminescent/adduct pair, a Förrester energy transfer pair and a dye dimer.

129. (Previously Presented) The probe of claim 116, wherein said probe comprises a detectable label.

130. (Previously Presented) The probe of claim 116, wherein said conditions include a temperature of about 60°C and a salt concentration of about 0.6 M to about 0.9 M.

131. (Previously Presented - Withdrawn) A method for determining the presence of SARS-CoV in a test sample, said method comprising the steps of:

a) contacting a test sample with said probe of claim 116 under said conditions; and

b) determining whether said hybrid is present in said test sample as indication of the presence of SARS-CoV in said test sample.

132. (Previously Presented - Withdrawn) The method of claim 131, wherein said target binding portion comprises an at least 10 contiguous base region which is perfectly complementary to an at least 10 contiguous base region of SEQ ID NO:3 or its complement.

133. (Previously Presented - Withdrawn) The method of claim 131, wherein said target binding portion comprises an at least 15 contiguous base region which is perfectly complementary to an at least 15 contiguous base region of SEQ ID NO:3 or its complement.

134. (Previously Presented - Withdrawn) The method of claim 131, wherein said target binding portion comprises an at least 18 contiguous base region which is perfectly complementary to an at least 18 contiguous base region of SEQ ID NO:3 or its complement.

Claims 135-138 (Canceled)

139. (Previously Presented - Withdrawn) The method of claim 131, wherein the base sequence of said probe is perfectly complementary to all or a portion of the base sequence of SEQ ID NO:3 or its complement.

140. (Previously Presented - Withdrawn) The method of claim 131, wherein the base sequence of said probe is perfectly complementary to 18 to 23 contiguous bases of the base sequence of SEQ ID NO:3 or its complement.

141. (Currently Amended - Withdrawn) The method of claim ~~135~~ 131, wherein said probe is a self-hybridizing probe under said conditions and in the absence of said target sequence.

142. (Previously Presented - Withdrawn) The method of claim 141, wherein said probe comprises a pair of interacting labels.

143. (Previously Presented - Withdrawn) The method of claim 142, wherein said pair of interacting labels is selected from the group consisting of a luminescent/quencher pair, a luminescent/adduct pair, a Förrester energy transfer pair and a dye dimer.

144. (Previously Presented - Withdrawn) The method of claim 131, wherein said probe comprises a detectable label.

145. (Previously Presented) A set of oligonucleotides for use in amplifying a target region present in SARS-CoV nucleic acid, said set comprising:

a first oligonucleotide up to 100 bases in length which binds to or extends through a first target sequence contained within SEQ ID NO:24 or its complement under amplification conditions; and

a second oligonucleotide up to 100 bases in length which binds to or extends through a second target sequence contained within SEQ ID NO:25 or its complement under amplification conditions.

146. (Previously Presented) The set of claim 145, wherein the base sequence of said first oligonucleotide is contained within a base sequence selected from the group consisting of SEQ ID NO:24, its complement, the DNA equivalents thereof, and any of the foregoing in combination with a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

147. (Previously Presented) The set of claim 145, wherein the base sequence of said second oligonucleotide is contained within a base sequence selected from the group consisting of SEQ ID NO:25, its complement, the DNA equivalents thereof, and any of the foregoing in combination with a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

148. (Previously Presented) The set of claim 146, wherein the base sequence of said second oligonucleotide is contained within a base sequence selected from the group consisting of SEQ ID NO:25, its complement, the DNA equivalents thereof, and any of the foregoing in combination with a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

149. (Previously Presented) The set of claim 145, wherein the base sequence of said first oligonucleotide consists of at least 18 contiguous bases of a base sequence selected from the group consisting of SEQ ID NO:24, its complement, the DNA equivalents thereof, and any of the foregoing in combination with a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

150. (Previously Presented) The set of claim 145, wherein the base sequence of said second oligonucleotide consists of at least 18 contiguous bases of a base sequence selected from the group consisting of SEQ ID NO:25, its complement, the DNA equivalents thereof, and any of the foregoing in combination with a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

151. (Previously Presented) The set of claim 149, wherein the base sequence of said second oligonucleotide consists of at least 18 contiguous bases of a base sequence selected from the group consisting of SEQ ID NO:25, its complement, the DNA equivalents thereof, and any of the foregoing in combination with a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

152. (Previously Presented) The set of claim 151, wherein at least one of said first and second oligonucleotides comprises a T7 promoter sequence.

153. (Previously Presented - Withdrawn) A method of amplifying a target region present in SARS-CoV nucleic acid, said method comprising the steps of:

a) contacting a test sample with said set of claim 145; and

b) exposing said test sample to amplification conditions such that said target region, if present in said test sample, is amplified.

154. (Previously Presented - Withdrawn) The method of claim 153, wherein the base sequence of said first oligonucleotide is contained within a base sequence selected from the group consisting of SEQ ID NO:24, its complement, the DNA equivalents thereof, and any of the foregoing in combination with a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

155. (Previously Presented - Withdrawn) The method of claim 153, wherein the base sequence of said second oligonucleotide is contained within a base sequence selected from the group consisting of SEQ ID NO:25, its complement, the DNA equivalents thereof, and any of the foregoing in combination with a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

156. (Previously Presented - Withdrawn) The method of claim 154, wherein the base sequence of said second oligonucleotide is contained within a base sequence selected from the group consisting of SEQ ID NO:25, its complement, the DNA equivalents thereof, and any of the foregoing in combination with a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

157. (Previously Presented - Withdrawn) The method of claim 153, wherein the base sequence of said first oligonucleotide consists of at least 18 contiguous bases of a base sequence selected from the group consisting of SEQ ID NO:24, its complement, the DNA equivalents thereof, and any of the foregoing in combination with a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

158. (Previously Presented - Withdrawn) The method of claim 153, wherein the base sequence of said second oligonucleotide consists of at least 18 contiguous bases of a base sequence selected from the group consisting of SEQ ID NO:25, its complement, the DNA equivalents thereof, and any of the foregoing in combination with a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

159. (Previously Presented - Withdrawn) The method of claim 157, wherein the base sequence of said second oligonucleotide consists of at least 18 contiguous bases of a base sequence

selected from the group consisting of SEQ ID NO:25, its complement, the DNA equivalents thereof, and any of the foregoing in combination with a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

160. (Previously Presented - Withdrawn) The method of claim 159, wherein at least one of said first and second oligonucleotides comprises a T7 promoter sequence.

161. (Previously Presented - Withdrawn) A method for determining the presence of SARS-CoV in a test sample, said method comprising the steps of:

a) contacting a test sample with said set of claim 145 under amplification conditions;

b) amplifying, if present in said test sample, said target region;

c) contacting said test sample a detection probe, said probe being up to 100 bases in length and comprising a target binding portion which forms a hybrid stable for detection with a target sequence contained within or complementary to a sequence contained within said target region under stringent hybridization conditions, wherein said probe does not form a hybrid stable for detection with nucleic acid derived from HCoV-OC43 or HCoV-229E under said stringent hybridization conditions; and

d) determining whether said hybrid is present in said test sample as indication of the presence of SARS-CoV in said test sample.

162. (Previously Presented - Withdrawn) The method of claim 161, wherein said target sequence is contained within the sequence of SEQ ID NO:3 or its complement under said stringent hybridization conditions, wherein said probe does not form a hybrid stable for detection with nucleic acid derived from HCoV-OC43 or HCoV-229E under said conditions.

163. (Previously Presented - Withdrawn) The method of claim 162, wherein said target binding portion comprises an at least 10 contiguous base region which is perfectly complementary to an at least 10 contiguous base region of SEQ ID NO:3 or its complement.

164. (Previously Presented - Withdrawn) The method of claim 162, wherein said target binding portion comprises an at least 15 contiguous base region which is perfectly complementary to an at least 15 contiguous base region of SEQ ID NO:3 or its complement.

165. (Previously Presented - Withdrawn) The method of claim 162, wherein said target binding portion comprises an at least 18 contiguous base region which is perfectly complementary to an at least 18 contiguous base region of SEQ ID NO:3 or its complement.

166. (Previously Presented - Withdrawn) The method of claim 162, wherein the base sequence of said target binding portion is perfectly complementary to all or a portion of the base sequence of SEQ ID NO:3 or its complement, and wherein said probe does not comprise any other base sequences which stably hybridize to nucleic acid derived from SARS-CoV under said stringent hybridization conditions.

167. (Previously Presented - Withdrawn) The method of claim 166, wherein said target binding portion comprises an at least 10 contiguous base region which is perfectly complementary to an at least 10 contiguous base region of SEQ ID NO:3 or its complement.

168. (Previously Presented - Withdrawn) The method of claim 166, wherein said target binding portion comprises an at least 15 contiguous base region which is perfectly complementary to an at least 15 contiguous base region of SEQ ID NO:3 or its complement.

169. (Previously Presented - Withdrawn) The method of claim 166, wherein said target binding portion comprises an at least 18 contiguous base region which is perfectly complementary to an at least 18 contiguous base region of SEQ ID NO:3 or its complement.

170. (Previously Presented - Withdrawn) The method of claim 162, wherein the base sequence of said probe is perfectly complementary to all or a portion of the base sequence of SEQ ID NO:3 or its complement.

171. (Previously Presented - Withdrawn) The method of claim 162, wherein the base sequence of said probe is perfectly complementary to 18 to 23 contiguous bases of the base sequence of SEQ ID NO:3 or its complement.

172. (Previously Presented - Withdrawn) The method of claim 162, wherein said probe comprises a detectable label.

173. (Previously Presented - Withdrawn) The method of claim 161, wherein said probe is provided to said test sample prior to or during said amplifying step.

174. (Previously Presented - Withdrawn) The method of claim 161, wherein at least a portion of said determining step occurs during said amplifying step.

175. (Currently Amended) A kit for use in determining the presence of SARS-CoV in a test sample, said kit comprising:

a first oligonucleotide up to 100 bases in length which binds to or extends through a first target sequence contained within the sequence of SEQ ID NO:24 or its complement under amplification conditions;

a second oligonucleotide up to 100 bases in length which binds to or extends through a second target sequence contained within the sequence of SEQ ID NO:25 or its complement under amplification conditions; and

a detection probe ~~up to 100 bases in length and~~ comprising a target binding portion ~~which forms a hybrid stable for detection with a target sequence contained within~~ that is perfectly complementary to all or a portion of a target sequence consisting of the base sequence of SEQ ID NO:3, ~~or~~ its complement,

wherein said target binding region forms a hybrid stable for detection with said target sequence under stringent hybridization conditions,

wherein said probe does not comprise any other base sequences which stably hybridize to nucleic acid derived from SARS-CoV under said conditions, and

wherein said probe does not form a hybrid stable for detection with nucleic acid derived from HCoV-OC43 or HCoV-229E under said stringent hybridization conditions.

176. (New) The probe of claim 116, wherein the base sequence of said target binding portion is perfectly complementary to the base sequence of SEQ ID NO:3 or its complement.

177. (New) The probe of claim 116, wherein the base sequence of said probe is perfectly complementary to the base sequence of SEQ ID NO:3 or its complement.

178. (New - Withdrawn) The probe of claim 131, wherein the base sequence of said target binding portion is perfectly complementary to the base sequence of SEQ ID NO:3 or its complement.

179. (New - Withdrawn) The probe of claim 131, wherein the base sequence of said probe is perfectly complementary to the base sequence of SEQ ID NO:3 or its complement.

180. (New - Withdrawn) The probe of claim 166, wherein the base sequence of said target binding portion is perfectly complementary to the base sequence of SEQ ID NO:3 or its complement.

181. (New - Withdrawn) The probe of claim 162, wherein the base sequence of said probe is perfectly complementary to the base sequence of SEQ ID NO:3 or its complement.